

48 kD G1-Untereinheit: präzessinär

## nucleic acid sequences

Fig

### G5 wild-type

DNAs in 0.2 M = 2.5 fmol DNA in 0.1

NU.44	10	20	30	40	50	60	70	80	90	100	110	120
	ATGAAATA ATATTGTTAT	ATATTGTTAT	ATTTCAATT	TTATCAATT	ATTTCAATT	ATTTCAATT	GTGTTTTC	CTGTTGAAAC	TTGAACTAC	ACACCGGT	ATGTTGATCA	TCGAGCT
130	140	150	160	170	180	190	200	210	220	230	240	
CCGCGAATT	CTGTTTAA	TTGAAAC	TTTATTAA	ATATTGTTAC	TCGTTGTT	CTGTTGCTA	GTGCTGTC	ACCTTGTC	TAAATTAAG	ATGTTGTC	TCGAGCT	
250	260	270	280	290	300	310	320	330	340	350	360	
CCACCTGTA	CTGCTATT	ATGCACTTA	TTGAACTTA	ATTTACGTT	AACTCCCTGC	TGTTACGCA	ATTCAGGGG	GAGGAACGA	TTATGAGCA	AAATGTTAA	TTCGAGTT	
370	380	390	400	410	420	430	440	450	460	470	480	
ATTTTTATA	ATGAAATTC	TCGAAATT	ATTCAGGGT	CTGTTACGTT	CACTGTTAC	CGGTTAAAC	GAATGTTGTC	TGGTTGACT	GCCTGTTAAT	CGCGTACCT	AGTCGCTAA	
490	500	510	520	530	540	550	560	570	580	590	600	
TCTAACCTG	CTGTCCTAC	TGTTACTGCA	CTGTTGTTG	GAATGTTAC	TGTTATGTT	AGATCATTTA	CAATGTTG	TAAATGTTGA	CTTAACTTT	ACTTAATGCG	TATATGTT	
610	620	630	640	650	660	670	680	690	700	710	720	
ATATCCTT	TCATTCAGG	TTAAAGTTA	TGCACTGTT	GTGCGGAT	TAACCTGAT	TAACCTGTT	ACCTAATGTT	GTCTACATTA	CGCTACATTA	CGCTACATTA	TAACCTGCA	
730	740	750	760	770	780	790	800	810	820	830	840	
TCGCCCTG	GTACTATAG	TGCTACCTCA	GTAAATTT	GGCTGACCA	AAACCTGA	TTGACTATT	GTGCTCCATA	CTTGTACAT	AAATATGCTC	CTTATTGTC	TCGCGTAT	
850	860	870	880	890	900	910	920	930	940	950	960	
AGTAACTGCC	TACCTTGCC	ACCAATTA	GTATTGTC	CTGAGCTTC	TGCAAGCTT	GCCTGCTT	TTGCACTTA	ATTTAATTT	GCATGCCCTA	ATGTTACCTC	ATTTGCTT	
970	980	990	1000	1010	1020	1030	1040	1050	1060	1070	1080	
GGAGGACTA	ATTTGTTAT	ATTTAAACA	GAATGTTAA	ATTTGTTAC	TTAATGTT	TTTATGTTA	TTTATGTTA	GGCTGGGTT	ATGTTGTC	ACCTGTC	ACCAAAAA	
1090	1100	1110	1120	1130	1140	1150	1160	1170	1180	1190	1200	
GTGTTAGCG	CTGTCGAC	TCGAGGTG	ACTCTACTT	TATTTGATA	ATTTGCTT	GTATGCCCT	GTGTTGTC	CTGCTACT	ACTTACCT	GTGAACT	CTTCTTAA	
1210	1220	1230	1240	1250	1260	1270	1280	1290	1300	1310	1320	
TGTGAACTG	TTTATGTC	TCGCAATT	TTATCTCA	ATTTCAAA	CTGAGCTCA	GGTTGAGCA	GTGTTGAA	CTGTTGAA	CTGTTGAA	AAATTTACTT	CTGCGCTCA	
1330	1340	1350	1360	1370	1380	1390	1400	1410	1420	1430	1440	
CTGTTGTC	CTTAAAAAA	TTTATTTG	GTATTGTC	ATTTTATC	TTTATGTTA							

Coding region: Nucleotides 1-1464

Fig. 2(a)

Coding region: nucleotides 1-1404

Fig. 2(b)

Sequence alignment of 48 kD G1 i-antigen  
and 55 kD G5 i-antigen protein sequences

SEQ 10 Nov: 6 G1  
SEQ 10 Nov: 7 G5

51 MKYILLIISLFINELRAVCPDGTQT-QAG-LTDVGAAIDLGTCVNCRPNFYYN---  
52 MKYINSLLITISLFIN---  
53 MKNNILVLLIISLFINIKSANCPVGETETNTAGQVDDLGTP--ANCVNCQKNFYYNNAA  
54 MKNNISLVLITISLFIN  
55 --GGAA---QGRANGNQF  
56 FVPGASTCTPCPQKKDAGAQPNPATANLVTQCNVKCPACTALAGGTDYAIITECVNC  
57 --P---AAN-NAARGICVCPQCINRUVGSVTNAGDLATLATQCS  
58 TQCTGTALDDGVTIPV  
59 RINFYNEAQNPNMAGASTCTACPVN  
60 FDRSAACQCVKCKPNFYNGSPQGEAPGVQVFAAGAAAAGVAAVTQSCVPCQLNK--NDS  
61 YVRSFTCVRKCRNFTYNGNIN--GNTP---FNP  
62 SOCTPCPAIKPANVA  
63 PATAGAQANLATQCSNQCPITVLDGVTLVENTSATLCKVCRPNFYYNGCSPQCEARGV  
64 QATLGNDATTAQCNVACPDGTISAAAGVN-NWVAQNTCTNCAPNFYYNN---AP--  
65 QVFAAGAAAAGVAAVTQSCVPCQINKND-SPATAGAQANLATQCS  
66 TQCTGTIAQDGATN  
67 VFSNSSTQCSOIANTFENG-NFEAGKSQLKCPVSKRTPAHAP-GNTATQATQCLTCP  
68 -WVLOTECLNAAANFYEDGNNFQAGSSRCKACPANKVQGAVATAGGTTLIAQCALECP  
69 AGTVLDDGTSNTNFVASATECTKCSAGFFASKTGTAGTUTCTRCTKLTSGATAKVAE  
70 AGTVLTDGTSYKQAASECVKCAANFYTQKQTMWAGIDTCTSCNQKLTSGAEANLPES  
71 AGTVQCASTTPEAKFLSISLFTISFYLL  
72 AKNNIQCD--PANFLSISLILLISYYLL  
73 FAKFLSISLLFLISFYLL  
74 FANFLSISLLIISYYLL  
75 FANFLSISLLIISYYLL  
76 FANFLSISLLIISYYLL  
77 FANFLSISLLIISYYLL  
78 FANFLSISLLIISYYLL  
79 FANFLSISLLIISYYLL  
80 FANFLSISLLIISYYLL  
81 FANFLSISLLIISYYLL  
82 FANFLSISLLIISYYLL  
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92 FANFLSISLLIISYYLL  
93 FANFLSISLLIISYYLL  
94 FANFLSISLLIISYYLL  
95 FANFLSISLLIISYYLL  
96 FANFLSISLLIISYYLL  
97 FANFLSISLLIISYYLL  
98 FANFLSISLLIISYYLL  
99 FANFLSISLLIISYYLL  
100 FANFLSISLLIISYYLL

Fig. 3(a)

## Sequence Alignment of 48 kD G1 i-antigen and 55 kD G5 i-antigen nucleotide sequences

G1	SEQ ID NO: 1	ATGAAATATAATTTTATTAAATTAAATTATTTTATTATTAATGAAATTAAAGAGCT
G5	SEQ ID NO: 3	ATGAAATATAATTTTATTAAATTAAATTATTTTATTATTAATGAAATTAAATCT
G1		GTTCCATGCTGATGGTACTTAGACTCA---AGCTGGAT---TGACTGATGAGGTGC
G5		CTTAATTTCTCTTCTGAACTGAACTAAACACAGCCGATAAGTTGA-TGATCTAGGAAC
G1		TGCTGATCTTCTGACTTTTGTAAATTGCG-AGACCTTAATTTTACTATAATGGTGGTGC
G5		TCCT-----GCAATTGTGTTAATTGTTAGAAA-AACTTTTATTATAATGCTGCTG
G1		CTTAAGGAGAAGCTAATGGAATTAACTTTGCGAGCAAATAATGCTGCTAGAGGTAAAT
G5		CTT-----TGTTCC-----TGGTGTAG---TACGT
G1		GTGTACCATG-CCA-AATAACAGA-GTAGGCTGTGTTACCAA-TGCAGGTG--ACTTAG
G5		GTACACTTGTCCATAAAAAAAAGATGCTGGTGTG-TAACCAATCCACCTGCTACT--G
G1		CTACTTTAGCCACATAATGCGACTTAAATGCTTACTGGCACTGCACTTGATGATGGAG
G5		CTAAATTAGTCACATAATGTAACGTTAAATGCCCTGTGGTACCCCAATTGCGGTGGTGG
G1		TGACAGATGTTTG--ATAGATCAGCCGCATAATGCTTAAATGCAAACCTAACCTTTA
G5		CARCAGATTATGCGAGCAATA-ATCA---CAGAATGTTAATTGTTAGAATTAAATTGTTA
G1		CTATAATGGTGGTTCTCTTAAGGTGAAGCTCTGGCGTTAAGTTTTGCTGCTGGTGC
G5		--TAATGA-----AA---ATGCTCC-----AAATTAA-----
G1		TGCCGCTGCAGGTGTTGCTGCCCTTACTGTTAAATGTTACCTTCCAACTAAACAAAAA
G5		-----TGCAAGGT-----CTAGTACATGACAGCTTCTGGTAAACAGAGT
G1		CGATTCCTGCCACTGCAGGT--GCCTAAGCTAAATTAGCCACATAATGTTAGCAATT
G5		TGGTGGTGCATTGACTGCTGGTAAATGCC---GCTACCATAGTCCGCAATAATGTAACGTCCC

Fig. 3(b)

G1	ATGTCCTACTGGCACTGTACTTGATGATGGACTGACACTTGTGTTAATACATGCCAC
G5	ATGTCCTACTGGCACTGTACTTGATGATGGACTGACACTTGTGTTAATACATGCCAC
G1	ATATGTTAAATGAGACCTAACTTTACTATAATGCT-----GGTT-----CTCCCTTA
G5	AGATGTTAAATGAGACCTAACTTTACTATAATGCTAATAATGGTAATACCTCCCTTA
G1	-----AGGTGAA-----GCTCTGGCGTTTA
G5	CAATCCAGTTAAAGTTATGCCACACCTTGTCCCGCAATTAACCTGCTAACTTCCCTTA
G1	AG-----TTT-----TTGC-----TGCTGG
G5	AGCTACTTACGTAATGATGCTACAATAACCGCATAATGTAACCTGCTATGCCCTGATG
G1	TGCT-----GCCGCTGCAG-----GTGTTGC-----
G5	TAATGCTAACTGCTGCTGGACTAAATTCGGTAGCCACAAAACACTGAAATGCTAAATG
G1	TGCTCTTAACTTTACAATAATAATGCTCTTAATTCGATCCAGTTAATAGCT
G5	-----TGCCGTTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT
G1	ACCTTGCCAAAATAACAAAACGATTCTCTG---CCACTGCGGGTGCCTAAGCTAAATT
G5	ACCTTGCCAGCAATAAGATTATGGTGTGCTGAGCCACTGCRGGTGTGCCGCTACTTT
G1	ACCCACATAATGAGACTTAATGTCACACTGGCACTGCAATT-CAAGACGGACTGACAC
G5	ACCCACATAATGTAATATGCACTGCTGATGGTACTGCAATTGCTACT-GGAGCAAC--
G1	TTGTTTTAGTAAT-TCATCCACATAATGTTCTTAAT-GCATTGCTAATTACTTTTTAA
G5	-TAATTTAT-CTAATTTATAACAGATGT-CTAATTGTCGCTGCTAATTGTTATTGTA
G1	TGGTAAT---TTCGAAGCAGGTAAAGTTAATGTTAAAG---TGTCCAGTAAGTAAACT
G5	TGGTAATTAATTTCTAGGCAAGGAAGTAGATGCC---AAGCCATGTCAGCAATAAGTT
G1	A-----CTCCAGCACATGCTCAGGTAAACTGCTACTTAAAGCCACATAATGTT---TT
G5	TAAGGGCTGTAGCAA---CTGCAGGGTACTGCTACTTTAATGCTATAATGCTCCCTT
G1	GACCACATGTCCTGCTGGTACAGTACTTGATGATGCCAACATCAACTAAATTGCTTC
G5	GA-----ATGCCCTGCTGGTACTGCTACTCACCGATGGAACACATCTACTTATAATAAGC
G1	CGCAACTGAAATGCTAAATGTTCTGCTGCCCTTTTGCTGATCAAAAACAACTGCTTTAC
G5	AGCATGTAATGTTAAATGTCGCTGCCAACTTTTAACTACAAAATAACTGATGGGT
G1	ACCAAGTACTGATACATGACTGAAATGACTAAAAAATTAACCTCTGGGCCACAGCTAA
G5	AGCAGGTTATGATACATGACTGAAATGACTGAAATTAACCTCTGGGCCACAGCTAA
G1	AGTATATGCTGAAAGCTACTGAAAG---TATAATGCGGCCCTCCACTACTTTGCTAAATT
G5	TTTAC---CTGAATCTGCTAAAAAAATATAATATAATGCTG-----ATTTGCTAAATT
G1	TTTATGATTTCTTATTTTATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT
G5	TTTATCAATTTCTTATTTATTTGATTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT

Fig 3(b)  
(cont)

65 kD i-antigen protein

10 20 30 40 50 60  
E6 10 N0:7 MKNNILVILI ISLFINQIKS ANC P V G T E T N T A G Q V D D L G T P A N C V N C Q K N F Y Y N N A A A F V  
70 80 90 100 110 120  
P G A S T C T P C P Q K K D A G A Q P N P P A T A N L V I Q C N V K C P A G T A I A G G A T D Y A A I I T E C V N C R I  
130 140 150 160 170 180  
N F Y N E N A P N F N A G A S T C T A C P V N R V G G A L T A G N A A T I V A Q C N V A C P T G T A L D D G V T T D Y V  
190 200 210 220 230 240  
R S F T E C V K C R L N F Y Y N G N N G N T P F N P G K S Q C T P C P A I K P A N V A Q A T L G N D A T I T A Q C N V A  
250 260 270 280 290 300  
C P D G T I S A A G V N N W V A Q N T E C T N C A P N F Y N N N A P N F N P G N S T C L P C P A N K D Y G A E A T A G G  
310 320 330 340 350 360  
A A T L A K Q C N I A C P D G T A I A S G A T N Y V I L Q T E C L N C A A N F Y F D G N N F Q A G S S R C K A C P A N K  
370 380 390 400 410 420  
V Q G A V A T A G G T A T L I A Q C A L E C P A G T V L T D G T T S T Y K Q A A S E C V K C A A N F Y T T K Q T D W V A  
430 440 450 460 470 480  
G I D T C T S C N K K L T S G A E A N L P E S A K K N I Q C D F A N F L S I S L L L I S Y Y L L \* \* . . . . .

Fig. 4

48 kDa G1 i-antigen repeats

SEQUENCE

	10	20	30	40	50	60	70	80	90
8	CFDQTOAQG	ITDVEAADLG	TCVLPFPNPFY	YEGGAAGGEA	NGKQFAPPEE	MLRGI	CVPCQDQKV	CEVTCQDIA	ELATOCSTI Q
9	CPGTAIIDDG	VTIDVFDHSAA	QCVVKCRPFPF	YNGGSPDGEA	PGVQVFAAGA	AAQGVAAVTS	QCVPCQDLSR	DEPATAGCQ	ELATOCSTI Q
10	CPGTAIIDDG	VTIVVESTISATI	LLVACRPPF	YNGGPPGEA	PGVQVFAAGA	AAQGVAAVTS	QCVPCQDLSR	DEPATAGCQ	ELATOCSTI Q
11	CPGTAIIDDG	VTIVVESTISATI	QGSQIATMYF	PGGEA	PGVQVFAAGA	AAQGVAAVTS	QCVPCQDLSR	DEPATAGCQ	ELATOCSTI F
12	CPGTAIIDDG	VTIVVESTISATI	ECVKOSAGFF	ASKTTG	PGVQVFAAGA	AAQGVAAVTS	QCVPCQDLSR	DEPATAGCQ	ELATOCSTI F

Fig. 5(a)

### 55 kDa G5 i-antigen repeats

SEQ 10 NW 551  
562  
573  
584  
595  
606

CRVGETTNTAGQDDLGTPANCVNQCKNFTYNNAA---AFVYPGCGSTCTPCPQKFDAGAQPNPPATAANLVT---QCNVK  
CPAGTAAITGG-ATDIAAIIITECVNCRINFYNNAP---NFNAGASTCTAChYVIRVGGALTAGNAATIV---AQCNVA  
CPITGTAALDDGVITDVRSEFTECVAFORLNFTYNNQDNPNGKSO---CIPCPAIPANVAOATLGNDAITTAQCNVA  
CPDGTESSAGYNNWAQN-TECINCAPNFTYNNAP---NFPGNSTOTPCPANDYGAFAATAGCAATLAK---QCNVA  
CRDGTAATPSGATNNVILQ-TECINCAANFYFDGN---NFOAGSSSCKACPANVQEAIAATAGCTTAQCNVA  
CPAGIVLTDGTTSTWKOASECVRCAANFYFTKQ---TDWVAGIDCTSCNKKITSGAAANLPESAKKNT---QCNVA  
\* \* \*

Fig. 5(b)

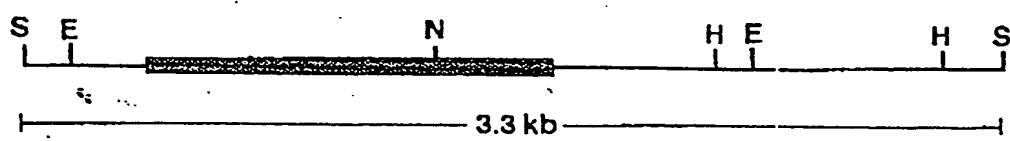
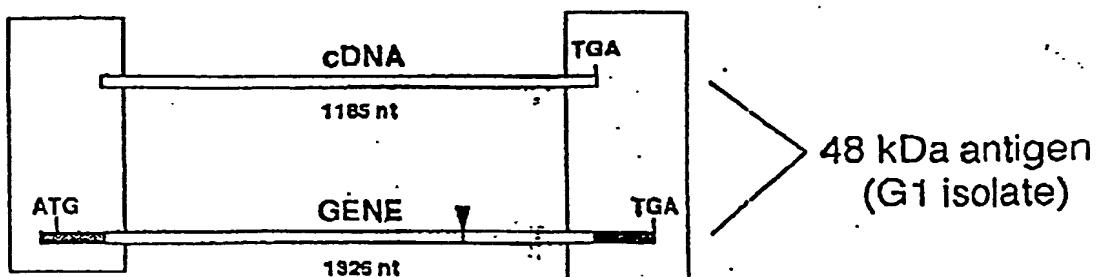
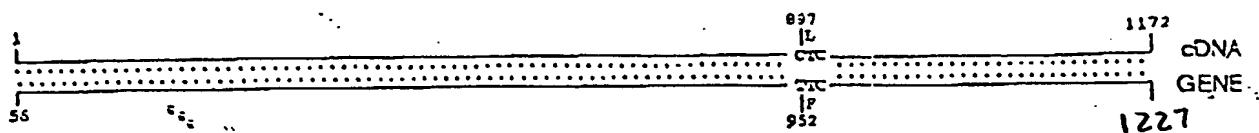


Fig. 6

A



B



C

Fig. 7

卷之三

SEE10W0161 i-ag 20 AVHPEDETOQAG-LTDVAGADLCTCNC-RPNFITYNGGAQG---EANGQD-PAANDAR--GIDP---CPINRVCSTVAGDLATL  
SEE10W0261 vBPA6-S1 61 AVDQP---GAGXYTDDGSVSDAKCCTKCDANGAATPILKCTKPSDETCG-SAGXYT-DSVSD  
SEE10W0361 vBPA6-S1 61 AVDQP---GAGXYTDDGSVSDAKCCTKCDANGAATPILKCTKPSDETCG-SAGXYT-DSVSD

i-ag  
vBPA6-51

i-ag  
vbpk6-S1

VLDGCTSTNEVAVASATCTTCAGGY----ASKTTGCT----AGTD-TCTCTTGTGATATAKVY--AKATOKVCLSTTPAK . 428  
NCADGQCTADVGGAKYCQDGKAPIDGCTAVAAAGRTNVACTADGCTCTCAGBYT-LMSGGCGVAKLPGKSWCLASRKR 459

88  
Fili

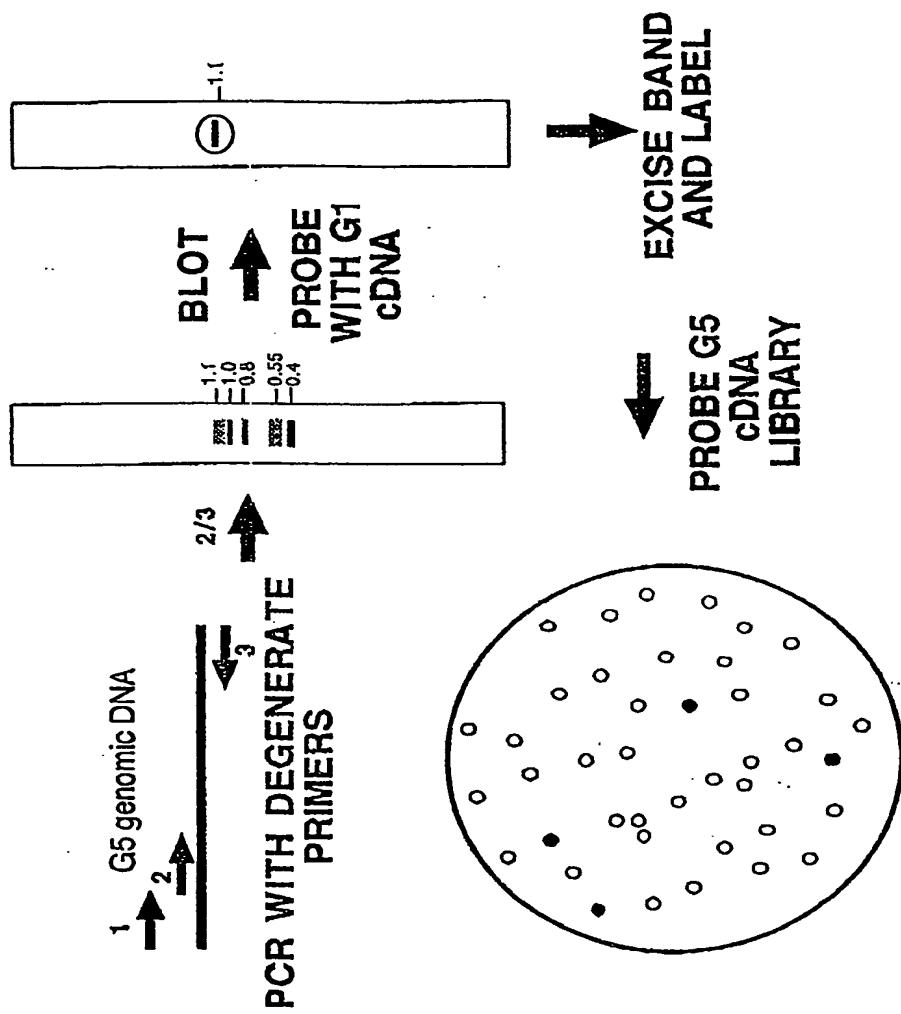


Fig. 9

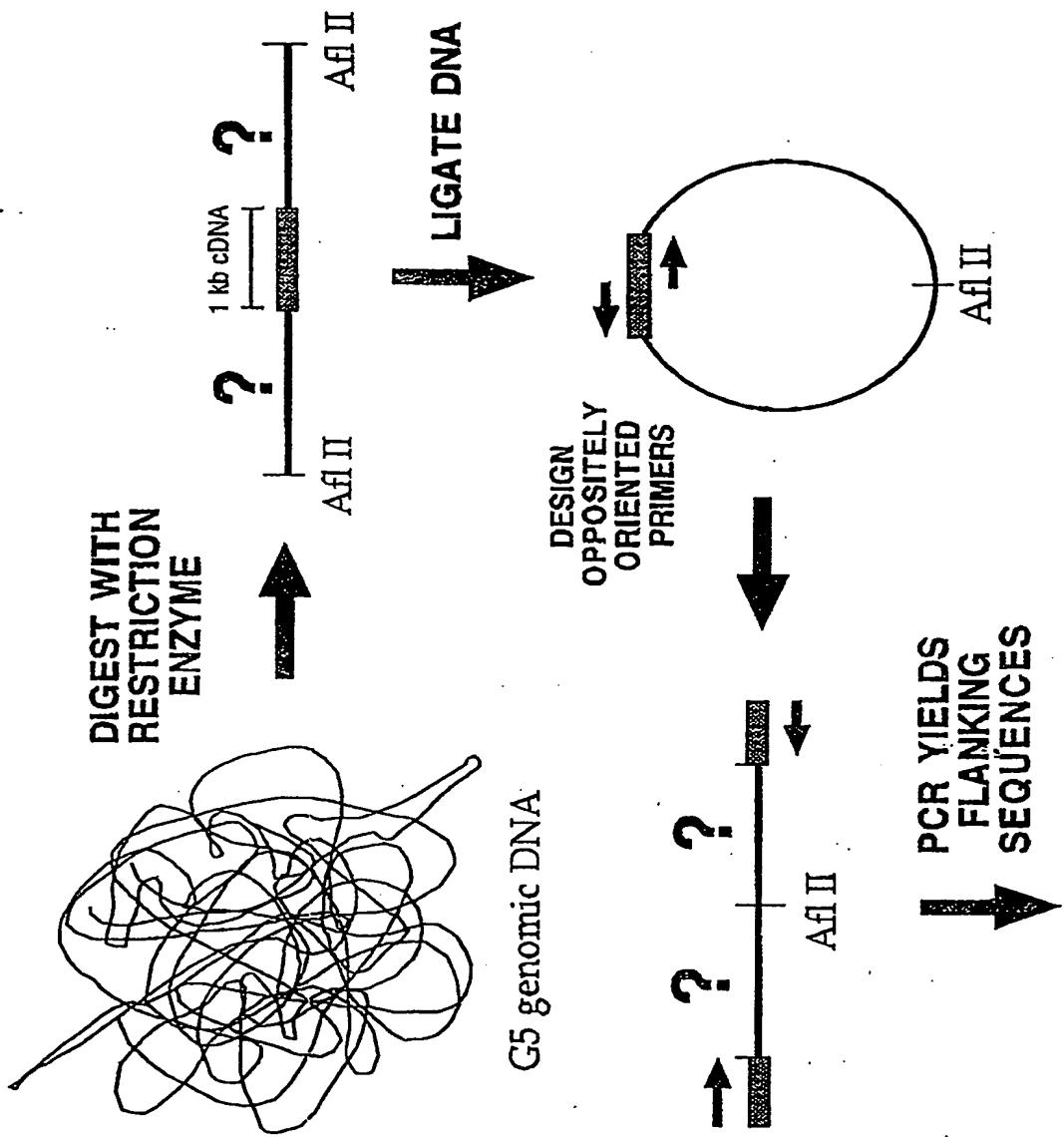


Fig. 10

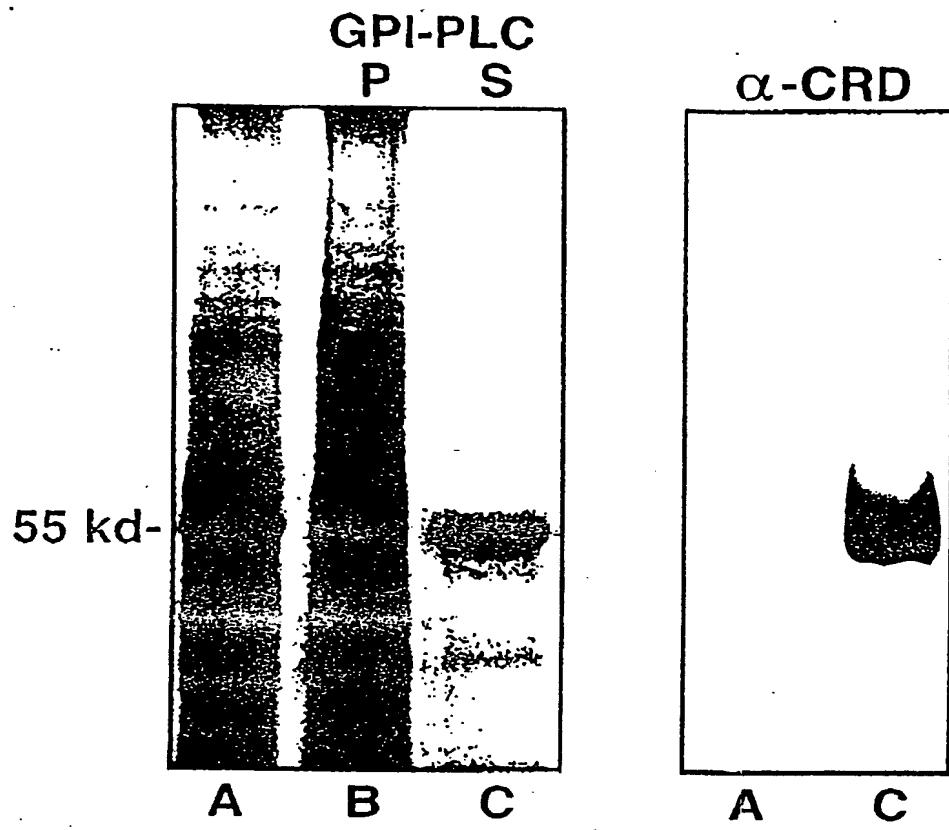


Fig. 11

SEQ. 10  
NO's Primers for synthesis of G5 synthetic gene.

70 3201:  
ATG GGA ATT CAA ATG AAG AAC AAC ATC CTG GTG ATC CTG ATC ATC TCT CTG TTC ATC AAC CAG ATC AAG  
TCT GCT AAC TGT CCT GTG GGA ACC GAG ACC AAC ACC GCT GGA CAG GTG  
3202:  
71 CTC CAG GCA CGA AAG CAG CAG CGT TGT TGT AGT AGA AGT TCT TCT GAC AGT TCA CAC AGT TAG CAG GGG  
TTC CCA GGT CGT CCA CCT GTC CAG CGG TGT TGG TC  
3203:  
72 CGC TGC TGC TTT CGT GCC TGG AGC TTC TAC CTG TAC CCC TTG TCC TCA GAA GAA GGA CGC TGG AGC TCA  
GCC TAA CCC TCC TGC TAC CGC TAA CCT GGT G  
3204:  
73 GAT GAT AGC AGC GTA GTC GGT AGC TCC TCC AGC GAT AGC GGT TCC AGC AGG ACA CTT CAC GTT ACA CTG  
GGT CAC CAG GTT AGC GGT AGC AGG AG  
3205:  
74 GCT ACC GAC TAC GCT GCT ATC ATC ACC GAG TGT GTG AAC TGT CGC ATC AAC TTC TAC AAC GAG AAC GCT  
CCT AAC TTC AAC GCT GGA GCT TCT ACC TGT ACC GCT TGT CCT GTG AAC CGC GTG GGA GGA GCT CTG ACC  
3206:  
75 GGT GAA AGA GCG CAC GTA GTC GGT GGT CAC TCC GTC GTC CAG AGC GGT TCC GGT AGG ACA AGC CAC GTT  
ACA CTG AGC CAC GAT GGT AGC AGC GTT TCC AGC GGT CAG AGC TCC TCC CAC GCG  
3207:  
76 GAC TAC GTG CGC TCT TTC ACC GAG TGT GTG AAG TGT CGC CTG AAC TTC TAC TAC AAC GGA AAC AAC GGA  
AAC ACC CCT TTC AAC CCT GGA AAG TCT CAG  
3208:  
77 GTG ATG GTA GCG TCG TTT CCC AGG GTA GCC TGA GCC ACG TTA GCA GGC TTG ATA GCA GGA CAA GGG GTA  
CACTGA GAC TTT CCA GGG TTG AAA GG  
3209:  
78 GGG AAA CGA CGC TAC CAT CAC CGC TCA GTG TAA CGT GGC TTG TCC TGA CGG AAC CAT CTC TGC TGC TGG  
AGT GAA CAA CTG GGT GGC TCA GAA C  
3210:  
79 CAG ACA GGT AGA GTT TCC AGG GTT GAA GTT AGG AGC GTT GTT GTT GAA GTT AGG AGC ACA GTT GGT  
ACA CTC GGT GTT CTG AGC CAC CCA GTT GTT C  
3211:  
80 CCC TGG AAA CTC TAC CTG TCT GCC TTG TCC TGC TAA CAA GGA CTA CGG AGC TGA GGC TAC CGC TGG AGG  
AGC TGC TAC CCT GGC TAA GC  
3212:  
81 GGT CTG CAG GAT CAC GTA GTT GGT AGC TCC AGA AGC GAT AGC GGT TCC GTC AGG ACA AGC GAT GTT ACA  
CTG CTT AGC CAG GGT AGC AGC  
3213:  
82 CAA CTA CGT GAT CCT GCA GAC CGA GTG TCT GAA CTG TGC TGC TAA CTT CTA CTT CGA CGG AAA CAA CTT  
CCA GGC TGG ATC TTC TCG CTG TAA GG  
3214:  
83 GAG CGA TCA GGG TAG CGG TTC CTC CAG CGG TAG CCA CAG CTC CCT GCA CCT TGT TAG CAG GAC AAG CCT  
TAC AGC GAG AAG ATC CAG CCT GG  
3215:  
84 GAA CCG CTA CCC TGA TCG CTC AGT GTG CTC TGG AGT GTC CTG CTG GAA CGG TGC TGA CGG ACG GAA CCA  
CCT CTA CCT ACA AGC AGG CTG CTC C  
3216:  
85 GGT GTC GAT TCC AGC CAC CCA GTC GGT CTG CTT GGT GGT GTA GAA GTT AGC AGC ACA CTT CAC ACA CTC  
AGA AGC AGC CTG CTT GTA GGT AG  
3217:  
86 GGG TGG CTG GAA TCG ACA CCT GTA CCT CTT GTA ACA AGA AGC TGA CCT CTG GAG CTG AGG CTA ACC TGC  
CTG AGT CTG CTA AGA AGA ACA TC  
3218:  
87 GAG GGA TCC TTA TTA CAG CAG GTA GTA AGA GAT CAG CAG CAG AGA GAT AGA CAG GAA GTT AGC GAA GTC  
ACA CTG GAT GTT CTT AGC AGA CT

Fig. 12

G5 proline mutant

10            20            30            40            50            60  
 NO.53 ATGAAGAAC A C A T C C C G G T G A T C A T C T C T G T T C A T C A A C C A G A T C A A G T C T  
 70            80            90            100            110            120  
 G C T A A C T G T C C T G G G A A C C G A G A C C A A C A C C G T G G A C G A G G T G G A C G A C C T G G G A A C C  
 130            140            150            160            170            180  
 C C T G C T A A C T G T G A A C T G T C A G A A G A A C T T C T A C T A C A A C A A C G C T G C T G C T G  
 190            200            210            220            230            240  
 C C T G G A G C T T C T A C C T G T A C C C T T G T C C T C A G A A G A A G G A C G C T G G A G C T C A G C C T A A C  
 250            260            270            280            290            300  
 C C T C C T G C T A C C G T A A C C T G T C C G T A A C G T G A A G T G T C C T G C T G G A A C C G C T  
 310            320            330            340            350            360  
 A T C G C T G G A G G A G C T A C C G A C T A C G C T G C T A T C A T C A C C G A G T G T G T G A A C T G C G C A T C  
 370            380            390            400            410            420  
 A A C T T C T A C A C C G A A C G A G A A C G C T C C T A A C T T C A C T C A A C G C T G G A G G C T I C T A C C T G T  
 430            440            450            460            470            480  
 C C T G T G A A C C G T G G G A G G A G C T C T G A C C G C C T G G A A A C G C T G C T A C C A T C G T G G C T C A G  
 490            500            510            520            530            540  
 T G T A A C G T G G C T T G C T A C C G C T G G A C C G A C G G A T G A C C A C A C G T A C A C G T G  
 550            560            570            580            590            600  
 C G C T C T T C A C C G A G T G T G T G T G A A G T G T C G C T G A A C T T C T C A T C A A C C G G A A A C A A C C G G A  
 610            620            630            640            650            660  
 A A C A C C C T T T C A A C C C T G G A A A G T C T C A G T G T A C C C T T G T C T G C T A T C A A G C C T G C T  
 670            680            690            700            710            720  
 A A C G T G G C T C A G G C T A C C C T G G A A G G A A C C G A C G C T A C C A T C A C C G T C A G T G G C T  
 730            740            750            760            770            780  
 T G T C C T G A C G G A A C C A T C T C T G C T G G A G T G A A C A A C T G G C T C A G A C A C C G A G  
 790            800            810            820            830            840  
 T G T A C C A A C T G T C T C T A A C T T C A A C A C A C G C T C T A A C T T C A A C C C T G G A A A C  
 850            860            870            880            890            900  
 T C T A C C T G T C T G C C T T G T C C T G C T A A C A A G G A C T A C G G A G G C T G A G G C T A C C C T G G A G G A  
 910            920            930            940            950            960  
 G C T G C T A C C C T G G C T A A G C A G T G T A A C A T C G C T T G T C C T G A C G G A A C C G C T A T C G C T T C T  
 970            980            990            1000            1010            1020  
 G G A G C T A C C A A C T A C G T G A T C C T G C A G G A C G A C C G A G T G T C T G A A C T T C T A C  
 1030            1040            1050            1060            1070            1080  
 T T C G A C G G A A C C A A C T T C C A G G C T G G A T C T C T G C T G T A A G G C T G T G C T C C T G C T A A C A A G  
 1090            1100            1110            1120            1130            1140  
 G T G C A G G G A G C T G G G C T A C C G C T G G A G G A A C C G C T A C C C T G A T C G C T C A G T G C T C T G  
 1150            1160            1170            1180            1190            1200  
 G A G T G T C C T G C T G G A C C G T G C T G A C C G A C G G A A C C A C C T C T A C C T A C A A G C A G G C T G C T  
 1210            1220            1230            1240            1250            1260  
 T C T G A G T G T G T G A A G T G T G C T G C T A A C T T C A C C A C C A A G C A G A C C G A C T G G G T G G C T

Fig. 13

proline mutant

1270 1280 1290 1300 1310 1320  
GGAATCGACA CCTGTACCTC TTGTAACAAG AAGCTGACCT CTGGAGCTGA GGCTAACCTG  
1330 1340 1350 1360 1370 1380  
CCTGAGCTG CTAAGAAGAA CATCCAGTGT GACTTCGCTA ACTTCCTGTC TATCTCTCTG  
1390 1400 1410 1420 1430 1440  
CTGCTGATCT CTTACTACCT GCTG.....

Fig 13 (cont'd)

G5 proline mutant protein

SEQ ID NO. 54

10	20	30	40	50	60																					
MKNNIPVILI	ISLFINQI	KSA	ANCPVGTEIN	TAGQVDDLGT	PANCVNCQKN	FYYNNAAFV																				
70	80	90	100	110	120																					
PGASTCTPCP	QKKDAGAQPN	PPATANLV	TQ	CNVKCPAGTA	IAGGATDYAA	IIITECVNCRI																				
130	140	150	160	170	180																					
NFYNENAPNF	NAGASTCTAC	PVN	RVGGALT	AGNAATIV	AQ	CNVACPTGTA	LDGVTTDYV																			
190	200	210	220	230	240																					
RSFTECVKCR	LNFYYNGN	NG	NTPFNP	GKSQ	CTPCPAIKPA	NVAQATLGND	ATITAQC	NVA																		
250	260	270	280	290	300																					
CPDG	TI	SAAG	VNNWVAQ	NTE	CTNCA	PNF	YFN	NNAP	NPN	GN	STCL	PCP	ANK	DYGA	EAT	AGG										
310	320	330	340	350	360																					
AATLAK	QC	NI	ACPD	GTA	I	AS	GAT	NYV	I	Q	L	T	E	C	L	N	CA	AN	FY	FDG	NNF	QAGS	SRCK	AC	P	ANK
370	380	390	400	410	420																					
VQG	A	VAT	AGG	TAT	LIA	QCAL	ECP	AGTV	LTD	GTT	STY	KQAA	SEC	VKCA	ANF	Y	TTK	QTD	WVA							
430	440	450	460	470	480																					
GID	TCT	SCNK	KLT	SGAE	AANL	PES	AKKNI	QC	DFAN	FLS	ISL	LLI	SY	YLL	...	.....	...	...	...							

Fig. 14

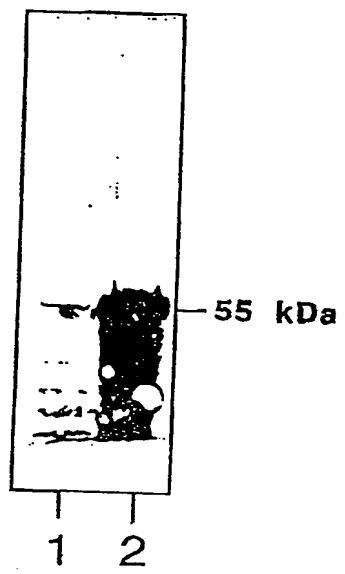


Fig. 15

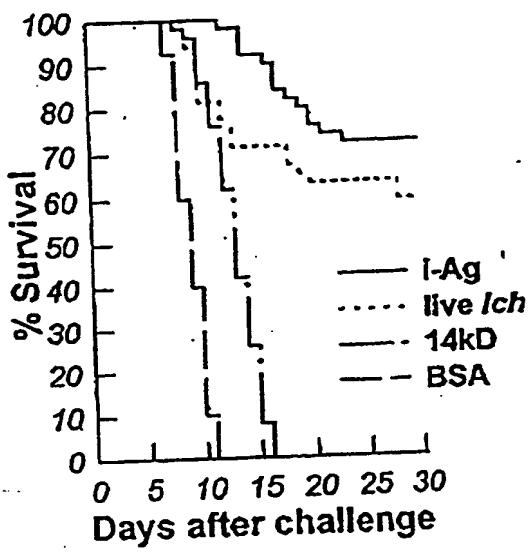


Fig. 16

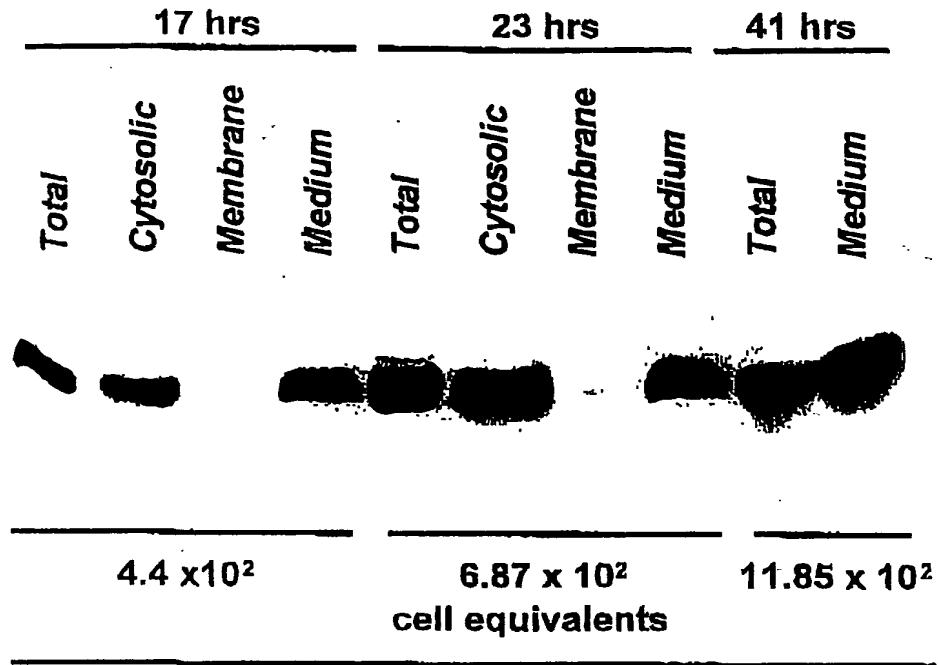


Fig. 17

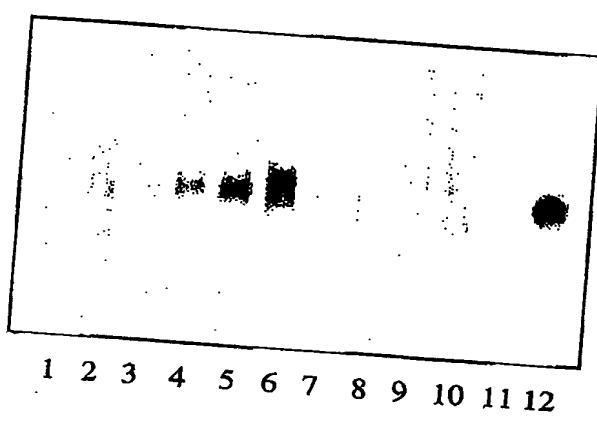


Fig. 1B

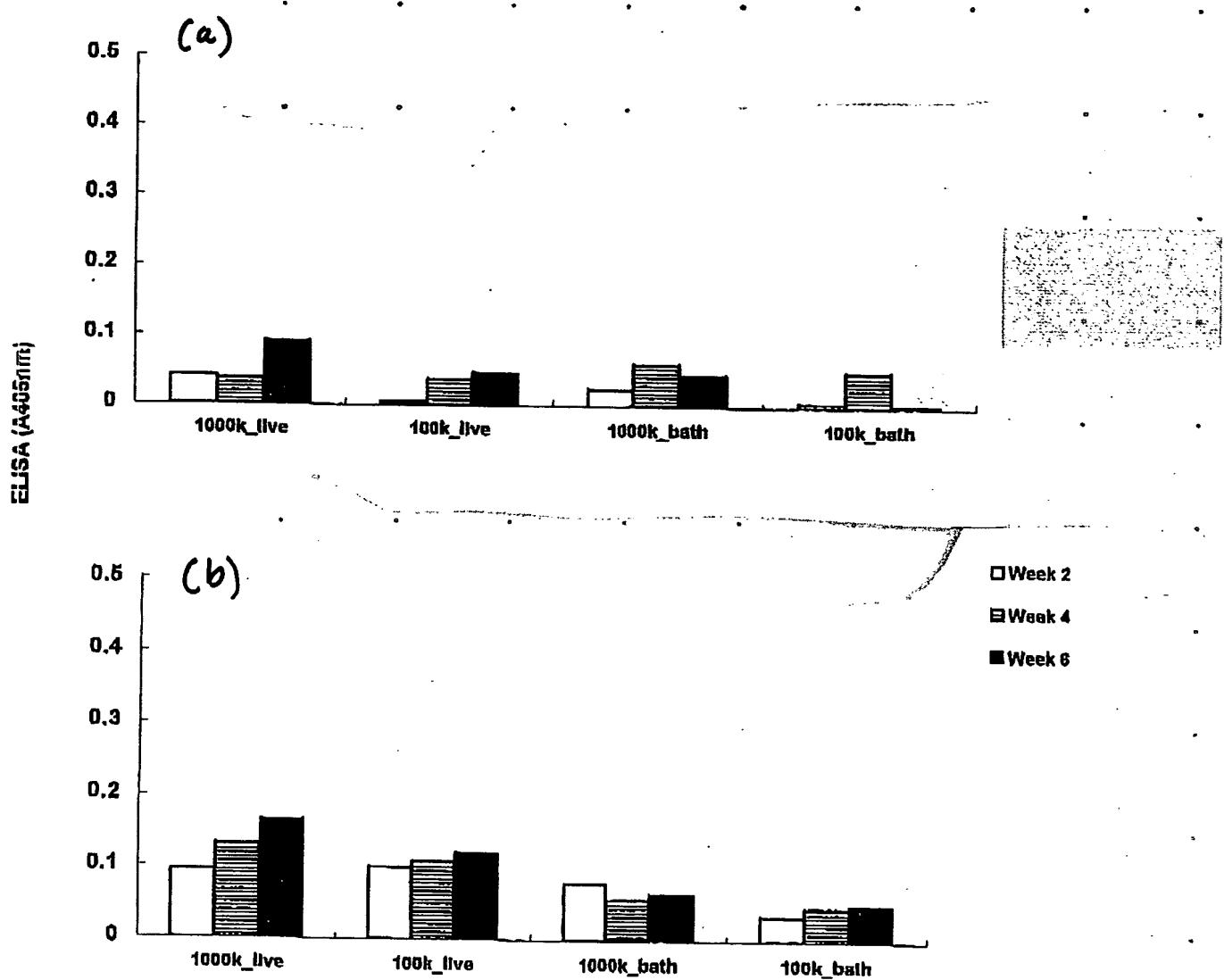
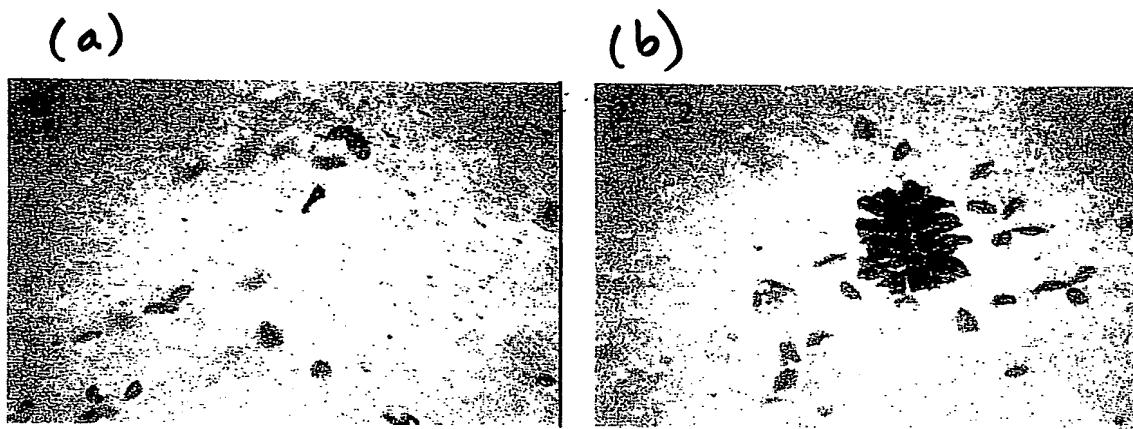


Fig. 19



Serum: anti-live Tneo (1 : 20)  
(negative control)

Serum: anti-live TG1 (1 : 20)

Fig. 20

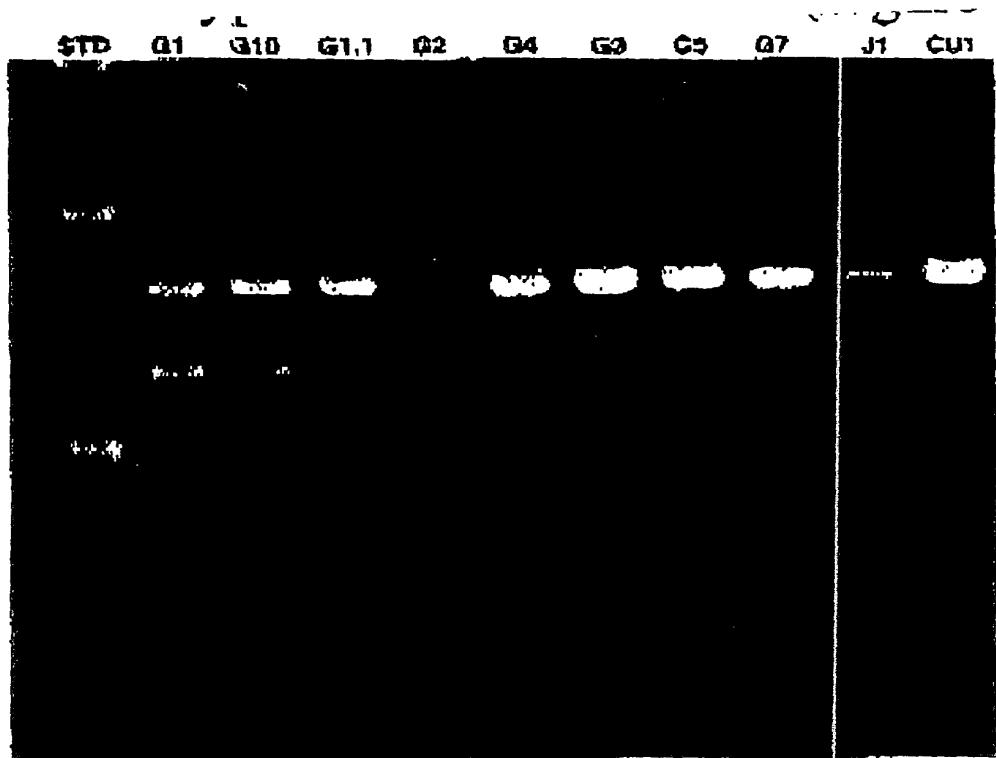


Fig. 2

Fig. 21